RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
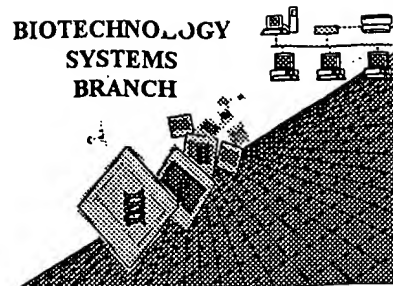BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/870,203_

Source: _O/PE_

Date Processed by STIC: _6/19/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 09/870,203

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
     prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
     ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
     each n or Xaa can only represent a single residue. Please present the maximum number of each
     residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
     Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
     This sequence is intentionally skipped

     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
     (NEW RULES)   <210> sequence id number
     <400> sequence id number
     000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
     is Artificial Sequence

     4 and more

11 ____ Use of <220>   Sequence(s) __4 and more__ missing the <220> "Feature" and associated numeric identifiers and responses.
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
     "Unknown." Please explain source of genetic material in <220> to <223> section.
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

DATE: 06/19/2001
TIME: 12:22:41 Does Not Comply
Corrected Diskette Needed

P.6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/870,203

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\06192001\I870203.raw

3 <110> APPLICANT: Novartis AG
5 <120> TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
7 <130> FILE REFERENCE: 4-31452A
9 <140> CURRENT APPLICATION NUMBER: US/09/870,203
C--> 9 <140> CURRENT FILING DATE: 2001-05-30
C--> 9 <141> NUMBER OF SEQ ID NOS: 43
9 <160> SOFTWARE: PatentIn version 3.0
11 <170>
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1746
15 <212> TYPE: DNA
16 <213> ORGANISM: Human adenovirus type 5
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (1)..(1746)
22 <400> SEQUENCE: 1
23 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48
24 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
25 1   5   10   15
27 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
28 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
29   20   25   30
31 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
32 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
33   35   40   45
35 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
36 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
37   50   55   60
39 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
40 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
41 65   70   75   80
43 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
44 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
45   85   90   95
47 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
48 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
49   100   105   110
51 act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
52 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
53   115   120   125
55 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
56 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
57   130   135   140
59 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
60 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
61 145   150   155   160
63 aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
64 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

6/19/01

file://C:\CRF3\Outhold\VsrI870203.htm

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/870,203   TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\06192001\I870203.raw

```
65                    165                  170                  175
67 gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg        576
68 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
69                    180                  185                  190
71 aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg        624
72 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
73           195                  200                  205
75 gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act        672
76 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
77      210                  215                  220
79 ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act        720
80 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
81 225                  230                  235                  240
83 gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca        768
84 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
85                    245                  250                  255
87 gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt        816
88 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
89                    260                  265                  270
91 agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag        864
92 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
93           275                  280                  285
95 ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac        912
96 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
97      290                  295                  300
99 aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag        960
100 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
101 305                  310                  315                  320
103 gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata       1008
104 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
105                   325                  330                  335
107 gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca       1056
108 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
109                   340                  345                  350
111 aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat       1104
112 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
113           355                  360                  365
115 tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac       1152
116 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
117      370                  375                  380
119 agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act       1200
120 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
121 385                  390                  395                  400
123 ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag       1248
124 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
125                   405                  410                  415
127 aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata       1296
128 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
129           420                  425                  430
```

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/870,203   TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\06192001\I870203.raw

```
131 ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata     1344
132 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
133         435                 440                 445
135 tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat     1392
136 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
137         450                 455                 460
139 gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt     1440
140 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
141 465                 470                 475                 480
143 aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga     1488
144 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
145                 485                 490                 495
147 ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc     1536
148 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
149             500                 505                 510
151 aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa     1584
152 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
153         515                 520                 525
155 cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac     1632
156 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
157         530                 535                 540
159 aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc     1680
160 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
161 545                 550                 555                 560
163 cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca     1728
164 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
165                 565                 570                 575
167 tac att gcc caa gaa taa                                             1746
168 Tyr Ile Ala Gln Glu
169             580
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 581
174 <212> TYPE: PRT
175 <213> ORGANISM: Human adenovirus type 5
177 <400> SEQUENCE: 2
179 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
180 1               5                   10                  15
183 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
184             20                  25                  30
187 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
188         35                  40                  45
191 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
192     50                  55                  60
195 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
196 65                  70                  75                  80
199 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
200                 85                  90                  95
203 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
204             100                 105                 110
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RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/870,203   TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\06192001\I870203.raw

```
207 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
208         115                 120                 125
211 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
212         130                 135                 140
215 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
216 145                 150                 155                 160
219 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
220                 165                 170                 175
223 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
224                 180                 185                 190
227 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
228         195                 200                 205
231 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
232         210                 215                 220
235 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
236 225                 230                 235                 240
239 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
240                 245                 250                 255
243 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
244                 260                 265                 270
247 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
248         275                 280                 285
251 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
252         290             .   295                 300
255 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
256 305                 310 ·               315                 320
259 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
260                 325                 330                 335
263 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
264                 340                 345                 350
267 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
268         355                 360                 365
271 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
272         370                 375                 380
275 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
276 385                 390                 395                 400
279 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
280             .   405                 410                 415
283 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
284         420                 425                 430
287 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
288         435                 440                 445
291 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
292         450                 455                 460
295 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
296 465                 470                 475                 480
299 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
300                 485                 490                 495
303 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
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RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/870,203   TIME: 12:22:41

Input Set : A:\4-31452A.ST25.txt
Output Set: N:\CRF3\06192001\I870203.raw

```
304              500              505              510
307 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
308          515              520              525
311 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
312      530              535              540
315 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
316 545              550              555              560
319 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
320              565              570              575
323 Tyr Ile Ala Gln Glu
324          580
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 1746
329 <212> TYPE: DNA
```
C--> 330 **<213> ORGANISM: Artificial**
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332 <220> FEATURE:
333 <223> OTHER INFORMATION: Codes for a mutated Human Adenovirus type 5 fiber protein.
335 <220> FEATURE:
336 <221> NAME/KEY: CDS
337 <222> LOCATION: (1)..(1746)
339 <220> FEATURE:
340 <221> NAME/KEY: mutation
341 <222> LOCATION: (1222)..(1227)
343 <400> SEQUENCE: 3
344 atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
345 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
346 1               5               10              15
348 tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
349 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
350          20              25              30
352 ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct     144
353 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
354          35              40              45
356 ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc     192
357 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
358      50              55              60
360 aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc     240
361 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
362 65              70              75              80
364 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac     288
365 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
366          85              90              95
368 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta     336
369 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
370          100             105             110
372 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc     384
373 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
374          115             120             125
376 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att     432
```

<210> 4
<211> 581
<212> PRT
<213> Artificial *per item 11 on Error Summary Sheet*

<400> 4

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : **A:\4-31452A.ST25.txt**
Output Set: **N:\CRF3\06192001\I870203.raw**

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L:9    M:270  C: Current Application Number differs, Replaced Current Application No
L:9    M:271  C: Current Filing Date differs, Replaced Current Filing Date
L:330  M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:496  M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:498  M:258  W: Mandatory Feature missing, <220> FEATURE:
L:498  M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:651  M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:815  M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:817  M:258  W: Mandatory Feature missing, <220> FEATURE:
L:817  M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:970  M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:1133 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:1135 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:1135 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1288 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:1452 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:1454 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:1454 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1607 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:1771 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:1773 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:1773 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1926 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:2092 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:2094 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:2094 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2247 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:2413 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:2415 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:2415 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2568 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:2732 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:2734 M:258  W: Mandatory Feature missing, <220> FEATURE:
L:2734 M:258  W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:2887 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:3051 M:220  C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
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